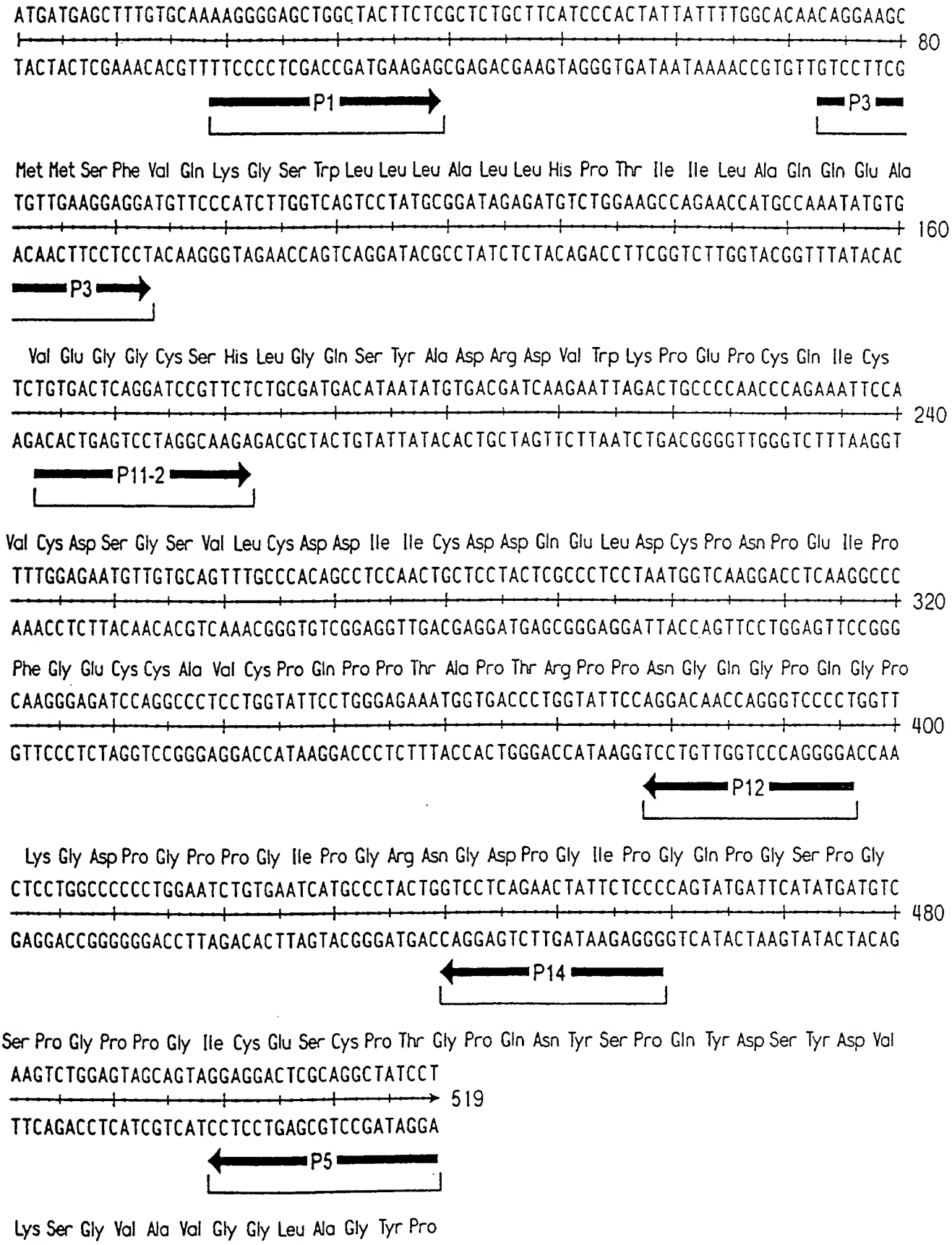
(78)

**Fig. 1**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P1
P3
Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala
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160
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P3
Val Glu Gly Gly Cys Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Gln Ile Cys
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240
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P11-2
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320
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Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro
CAAGGGAGATCCAGGCCCTCCTGGTATTCCTGGGAGAAATGGTGACCCTGGTATTCCAGGACAACCAGGGTCCCCTGGTT
400
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P12
Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln Pro Gly Ser Pro Gly
CTCCTGGCCCCCCTGGAATCTGTGAATCATGCCCTACTGGTCCTCAGAACTATTCTCCCCAGTATGATTCATATGATGTC
480
GAGGACCGGGGGGACCTTAGACACTTAGTACGGGATGACCAGGAGTCTTGATAAGAGGGGTCATACTAAGTATACTACAG
P14
Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val
AAGTCTGGAGTAGCAGTAGGAGGACTCGCAGGCTATCCT
519
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P5
Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro

**Fig. 2**

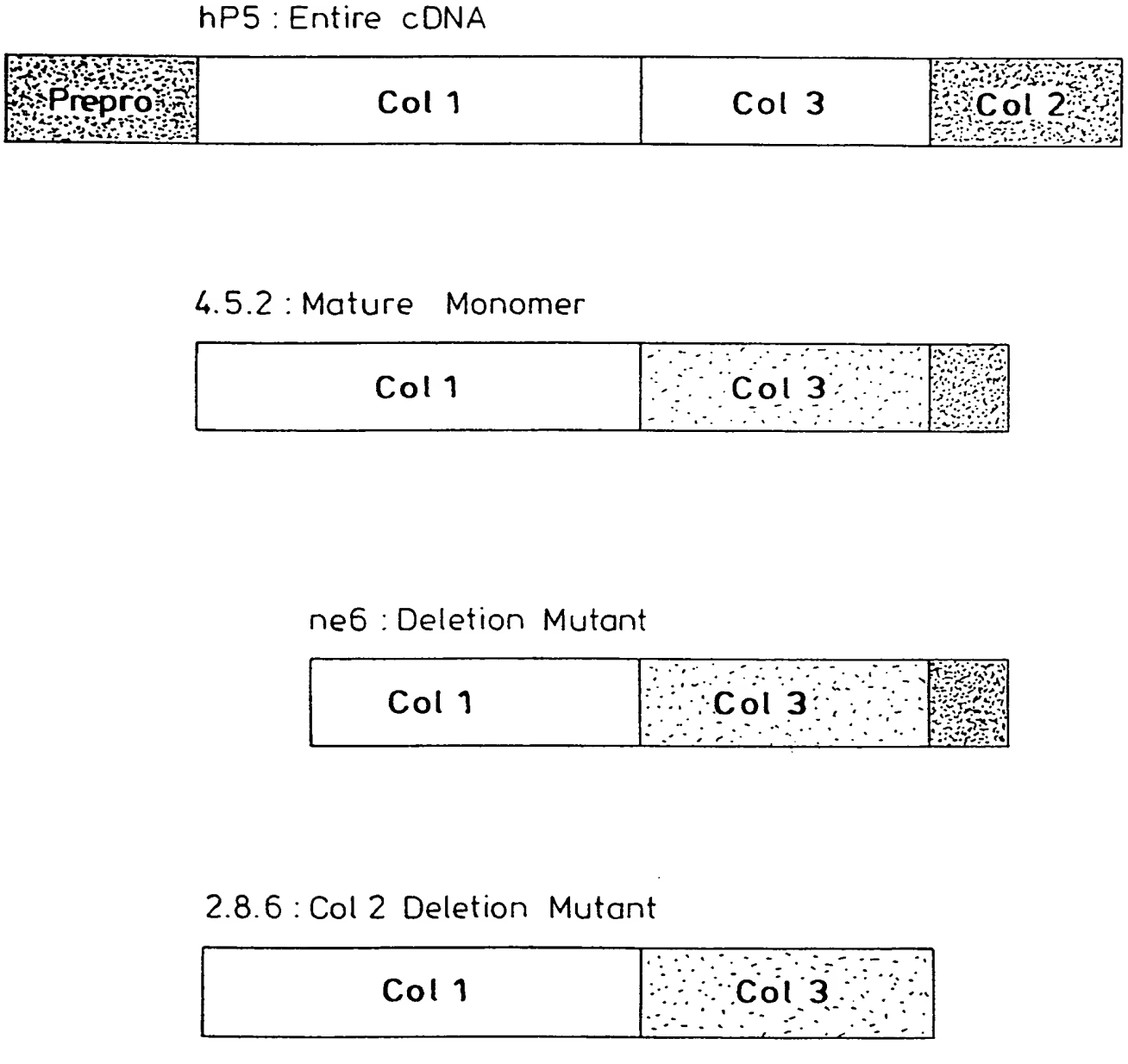

hP5 : Entire cDNA
Prepro
Col 1
Col 3
Col 2
4.5.2 : Mature Monomer
Col 1
Col 3
ne6 : Deletion Mutant
Col 1
Col 3
2.8.6 : Col 2 Deletion Mutant
Col 1
Col 3

**Fig. 3**

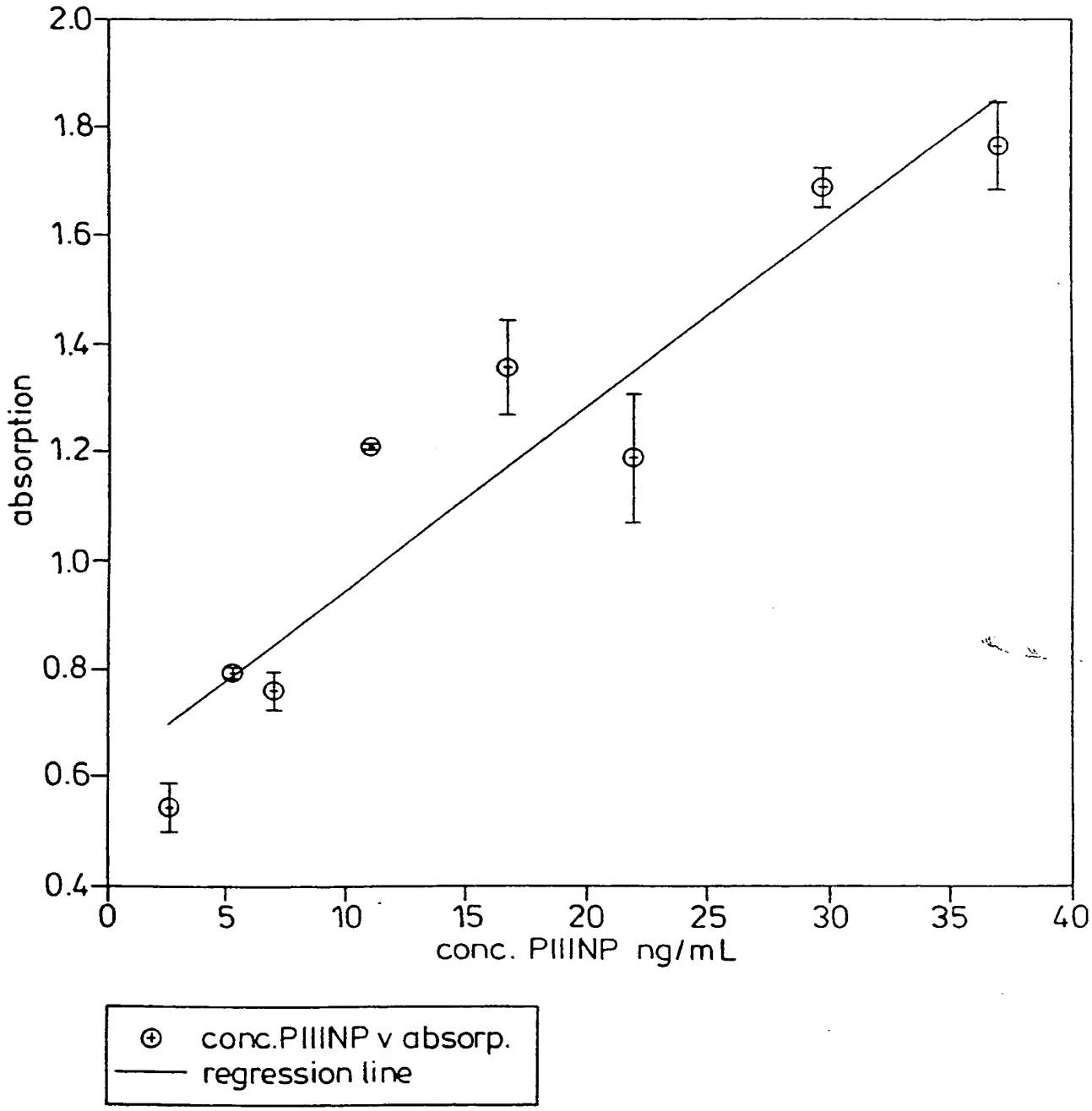
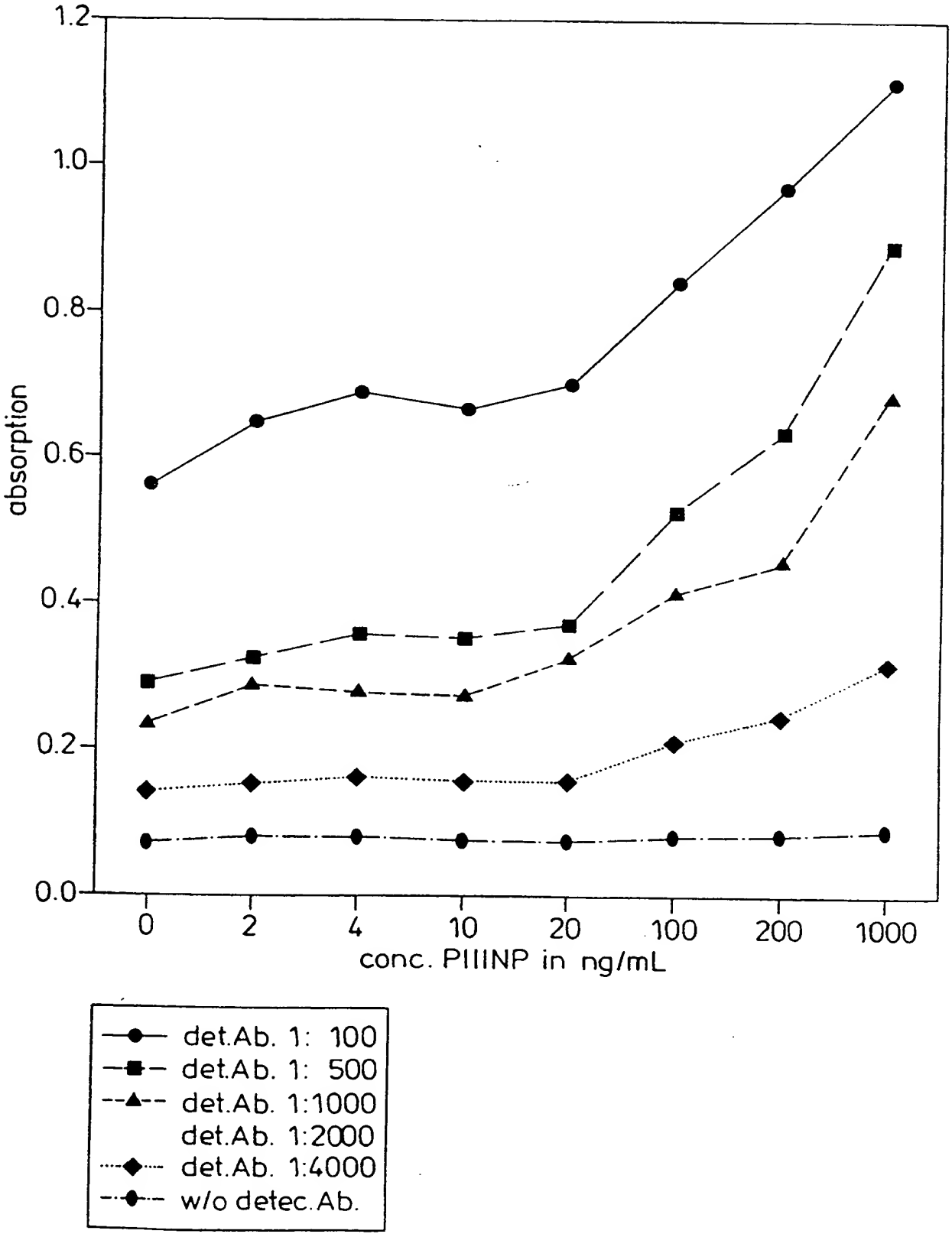

2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
absorption
0
5
10
15
20
25
30
35
40
conc. PIIINP ng/mL
conc.PIIINP v absorp.
regression line

**Fig. 4**


1.2
1.0
0.8
0.6
0.4
0.2
0.0
absorption
0
2
4
10
20
100
200
1000
conc. PIIINP in ng/mL
det.Ab. 1: 100
det.Ab. 1: 500
det.Ab. 1:1000
det.Ab. 1:2000
det.Ab. 1:4000
w/o detec.Ab.